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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/061,043	01/30/2002	David J. Glass	REG753B	8223

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EXAMINER	
KERR, KATHLEEN M	

ART UNIT	PAPER NUMBER
1652	

DATE MAILED: 04/16/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/061,043	GLASS ET AL.	
	Examiner	Art Unit	
	Kathleen M Kerr	1652	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *06 February 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-3,5-8 and 33-40* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3,5-8 and 33-40* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *3/17/03*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *alignments*. (3)

DETAILED ACTION

Application Status

1. In response to the previous Office action, a written restriction requirement (mailed on January 21, 2004), Applicants filed a response and amendment received on February 6, 2004. Said amendment cancelled Claims 4 and 9-32, amended Claims 1-3, 5, and 6, and added new Claims 33-40. Thus, Claims 1-3, 5-8, and 33-40 are pending in the instant Office action.

Election

2. Applicant's election of Group III, Claims 1-3 and 5-8 related to SEQ ID NO:34 in a paper received on February 6, 2004 is acknowledged. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (M.P.E.P. § 818.03(a)). Applicants have amended Claims 1-3 and 5-8 to be limited to the elected subject matter. Moreover, new Claims 33-40 would fall within the elected Group and will be examined herein. Thus, Claims 1-3, 5-8, and 33-40 are pending in the instant application and will be examined herein.

Information Disclosure Statement

3. The information disclosure statement filed on March 17, 2003 has been reviewed, and its references have been considered as shown by the Examiner's initials next to each citation on the attached copy.

Compliance with the Sequence Rules

4. By virtue of the sequence listing filed on January 27, 2003, in computer readable form and paper copy containing 48 sequences, the instant application now fully complies with the sequence rules.

Objections to the Specification

5. The specification is objected to because the title is not descriptive. A new title is required that is clearly indicative of the invention to which the elected claims are drawn (see M.P.E.P. § 606.01). The Examiner suggests the following new title:

---Nucleic Acid Molecules encoding MAFBX, a protein related to Ubiquitin Ligase---

6. In the specification, the Abstract is objected to for not completely describing the disclosed subject matter (see M.P.E.P. § 608.01(b)). It is noted that in many databases and in foreign countries, the Abstract is crucial in defining the disclosed subject matter, thus, its completeness is essential. The Examiner suggests the inclusion of the specific source species, human and rat, for completeness. Also, the term "MAFBXpathw" at the end of the Abstract is unclear and may be a typographical error. Correction and/or clarification are required.

7. The specification is objected to for being confusing concerning the nature of MA-61 and MAFBX. The terms seem to be used interchangeable. If they are, in fact, the same protein, a statement to that effect is required in the Abstract and in their first occurrence in the specification.

8. The specification is objected to for having improper citations as follows:

a) On page 3, line 27, "Winston, 1999" must identify ---*supra*--- to indicate that the full citation can be found earlier in the specification.
b) On page 4, line 9, the citation of "Newey, in press" is incomplete and, thus, an improper incorporation by reference (see first paragraph of the specification); deletion is required.
c) On page 49, line 14, the citation of Kipreos is incomplete; completion is required and amendable since the complete reference is indicated clearly by the incomplete citation.

Correction is required for all of the above points.

9. The specification is objected to for the following unclear use of sequence numbers:

a) On page 12, the description of Figure 4. These numbers seem indicative of residues of a protein, but the specific protein referred to is unclear and should be referred to by name as well as SEQ ID NO.
b) On page 45, line 31. Reference to residue numbers is found without any reference to the specific sequence (SEQ ID NO) to which they are related.
c) On pages 47-48, bridging paragraph. Reference to nucleotide numbers is found without any reference to the specific sequence (SEQ ID NO) to which they are related.
d) On pages 54, line 3. Reference to nucleotide numbers is found without any reference to the specific sequence (SEQ ID NO) to which they are related.

Correction is required for all of the above points.

10. The specification is objected to for having unclear descriptions of and/or references to

Figures as follows:

a) On page 13, the description of Figure 13 is confusing because the figure actually names the sequence SEQ ID NO:10 while the description notes the sequences as SEQ ID NO:27.
b) On pages 14-15, the description of Figures 27-31 is unclear. The first sentence describes Figure 27A and the second describes Figure 27B; both sentences do not describe both 27A and 27B as written. This confusion is reiterated for Figures 28-31.
c) On page 42, line 4, reference to Figure 1A is confusing since no Figure 1A is in the specification.
d) On page 43, references to Figures 2B, 2C, and 2D are confusing since only one panel in Figure 2 is found.

e) On page 45, references to Figures 3A and 3B are confusing since only one panel in Figure 3 is found.
f) On page 47, references to Figure 4C are confusing since only one panel in Figure 4 is found. On page 49, references to Figure 4B are confusing since only one panel in Figure 4 is found.
g) On pages 50 and 51, references to Figures 5B-C and 6A-C are unclear.
h) On the noted pages, references to Figures 27-31 as, for example, "Figures 27A-27BA" and "Figures 27A-27BB" are confusing since these Figures are A-B and not BA or BB. Pages 42, 43, 45, 46, and 52-54.
i) On page 45, line 8, the notation of "right" is unclear if not specifically referring to a figure.
j) On page 49, line 34, reference to Figure 5A is incorrect; the correct reference is to Figure 27A. This same correction is necessary on page 50, line 35.

Correction on all of the above points is required.

11. The specification is objected to for not having updated US patent information. On page 55, reference to a US application, 09/732,234, must be updated to the USPN 6,586,251. Correction is required.

12. The specification is objected to for improper citation of a trademark. On page 7, line 32, the use of the trademark "Taqman" has been noted. It should be capitalized wherever it appears and be accompanied by the generic terminology.

Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner, which might adversely affect their validity as trademarks.

Claim Objections

13. Claims 2 are objected to for improper format of a Markush group. In Claim 1, items a and b must be linked by the conjunction ---and--- (as filed, no conjunction is in the claim) to

identify the group selected from. In Claim 2, items b and c must be linked by the conjunction ---and--- (as filed, "or" is in the claim between items b and c) to identify the group selected from. Correction is required.

14. Claim 3 is objected to under 37 C.F.R. § 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. The parent claim, Claim 1, requires an exact sequence, within the degeneracy of the genetic code while Claim 3 limits to any molecule that hybridizes under particular conditions without any limitation of encoding.

Claim Rejections - 35 U.S.C. § 112

The following is a quotation of the second paragraph of 35 U.S.C. § 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

15. Claims 2 and 5-8 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The structure of the preamble is confusing. The requirement to encode "MAFBX" is unclear since only one sequence, SEQ ID NO:35, is disclosed as MAFBX; however, the scope of the variation of items b and c indicate that SEQ ID NO:35 need not be exactly encoded to meet all the limitations of the claim. In the preamble, it is also unclear if the fragment is limited by the requirements of a-c or if a fragment of something meeting the limitations of a-c is all that is required.

The term "stringent conditions" is unclear. On page 6, the specification describes what stringent conditions "may include" but a definite statement of what these conditions are is lacking in the specification and/or the claims.

The "biological activity of MAFBX" is unclear. On page 1, MA-61 (another apparent name for MAFBX) is described as "novel substrate-targeting subunits of ubiquitin ligases"; however, a definite function is not ascribed to MAFBX. Acting as a subunit is not considered a function of a molecule. If some binding function and/or some catalytic function is required to be an MAFBX, such function(s) should be made clear.

Item (c) is wholly confusing. Is the phrase "but for the degeneracy of the genetic code" intended to mean that that nucleotide sequence of item c does not hybridize but if it were altered within the degeneracy of the genetic code it now would hybridize? Also, the term "hybridize" used in item c has no definition; the Examiner notes that all nucleotide sequences hybridize to some extent to each other based on their inherent polar nature.

Clarification on all these points is required.

16. Claims 3 and 33-36 are rejected under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The phrase "derived from" is unclear. Must the nucleic acid molecules claimed be native to a mammalian genome? The term "derived from" can indicate recombinant biology techniques to alter a sequence wherein this phrase does not limit to molecules that are mammalian in origin.

The term "stringent conditions" is unclear. On page 6, the specification describes what stringent conditions "may include" but a definite statement of what these conditions are is lacking in the specification and/or the claims.

The inclusion of a ring domain is confusing in a molecule related to MAFBX since MAFBX is disclosed as having an F-box domain, not a ring domain as found in MURF1 and MURF3 (see page 4). Moreover, the structure of a ring domain is unclear since the specification provides only functional description (see page 3).

Clarification on all these points is required.

The following is a quotation of the first paragraph of 35 U.S.C. § 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

17. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 112, first paragraph, written description, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The instant claims are drawn to nucleic acid molecules encoding MAFBX polypeptides with unclear functional limitations and limited and/or unclear structural limitations.

The Court of Appeals for the Federal Circuit has recently held that a "written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as be structure, formula [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." University of California v. Eli Lilly and

Co., 1997 U.S. App. LEXIS 18221, at *23, quoting Fiers v. Revel, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993) (bracketed material in original). To fully describe a genus of genetic material, which is a chemical compound, applicants must (1) fully describe at least one species of the claimed genus sufficient to represent said genus whereby a skilled artisan, in view of the prior art, could predict the structure of other species encompassed by the claimed genus and (2) identify the common characteristics of the claimed molecules, e.g., structure, physical and/or chemical characteristics, functional characteristics when coupled with a known or disclosed correlation between function and structure, or a combination of these.

In the instant specification, a nucleic acid molecule encoding MAFBX is described in the form of SEQ ID NO:34, which encodes SEQ ID NO:35, a 355 amino acid protein. The specification fully describes the genus relating to said SEQ ID NOs with sequence identity limitations. However, the absence of clear structural limitations and clear functional limitations renders the instant claims broad enough to encompass virtually any DNA sequence with a mild affinity for SEQ ID NO:34. The genus of the instant claims contains polynucleotides within the sequence identity limitations, but having different function, and the specification does not describe such polynucleotides. Applicants have not fully described a genus that has sequence identity limitations in the absence of functional limitations.

The Examiner suggests clear structural and functional limitations on the claimed nucleic acid molecules to overcome the instant rejection.

18. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 112, first paragraph, scope of enablement, because the specification, while being possibly enabling nucleic acid molecules that encode SEQ ID NO:35, does not reasonably provide enablement for nucleic acid molecules with

some structural (although unclear) and functional (also unclear) relationship to SEQ ID NO:34/35. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make the invention commensurate in scope with these claims. To make the claimed nucleic acid molecules to the full extent of the claimed scope would require undue experimentation.

The factors to be considered in determining whether undue experimentation is required are summarized In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988). The Court in Wands states: "Enablement is not precluded by the necessity for some experimentation such as routine screening. However, experimentation needed to practice the invention must not be undue experimentation. The key word is 'undue,' not 'experimentation.' " (Wands, 8 USPQ2d 1404). Clearly, enablement of a claimed invention cannot be predicated on the basis of quantity of experimentation required to make or use the invention. "Whether undue experimentation is needed is not a single, simple factual determination, but rather is a conclusion reached by weighing many factual considerations." (Wands, 8 USPQ2d 1404). The factors to be considered in determining whether undue experimentation is required include: (1) the quantity of experimentation necessary, (2) the amount or direction or guidance presented, (3) the presence or absence of working examples, (4) the nature of the invention, (5) the state of the prior art, (6) the relative skill of those in the art, (7) the predictability or unpredictability of the art, and (8) the breadth of the claims. While all of these factors are considered, a sufficient amount for a *prima facie* case is discussed below.

Applicants present no guidance or working examples of the use of polynucleotides that have such low sequence identity with respect to SEQ ID NO:34. The nature of the invention is

such that the DNA encodes a functional protein, an MAFBX involved in ubiquitination; and with such a great deviation from the known sequence, the predictability of functionality becomes extremely low. Such enormous breadth and unpredictability renders the instant claims not enabled to the full extent of their scope without undue experimentation. Additionally, the instant specification teaches SEQ ID NO:35, an MAFBX ubiquitin ligase subunit protein from human, and SEQ ID NO:34, a human gene exactly encoding SEQ ID NO:35. The art includes no examples of MAFBX encoding genes. The art fully enables any DNA encoding SEQ ID NO:35 based on the degeneracy of the genetic code. While the instant specification describes and enables means for identifying other MAFBX genes using hybridization methods, etc., these methods do not enable one of skill in the art to make all, or a relevant portion of, the polynucleotides within the scope of the claims because the ability to find a MAFBX gene, which is structurally related to SEQ ID NO:34, is not equivalent to the ability to make an MAFBX gene as required by the statute (i.e., "make and use"). No description in the specification or the art provides particular residues whose encoding is important within the disclosed sequence so that its MAFBX-nature is maintained. Thus, one of skill in the art would be unable to predict the structure of the other members of the genus in order to make such members. Therefore, the instant claims are not enabled to the full extent of their scope.

19. Claims 7-8 are rejected under 35 U.S.C. § 112, first paragraph, scope of enablement, because the specification, while being possibly enabling host-vector systems for the production of MAFBX wherein an expression vector is used, does not reasonably provide enablement for systems wherein a vector other than an expression vector is used. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly

connected, to make the invention commensurate in scope with these claims. To make host vector systems for expression in the absence of expression vectors would require undue experimentation as summarized in the Wands factors above.

The nature of the host-vector system claimed is the MAFBX protein production is required. Expression vectors, such as found in Claims 6, 34, and 38, are appropriate for such systems. The specification has not taught, by way of examples or guidance, how to produce host-vector systems that produce MAFPX in the absence of expression vectors. Thus, the specification has not taught how to make the full scope of the claimed invention.

Claim Rejections - 35 U.S.C. § 101

35 U.S.C. § 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

20. Claims 1-3, 5-8, and 33-40 are rejected under 35 U.S.C. § 101 because the claimed invention lacks patentable utility. To fulfill the utility requirement of 35 U.S.C. § 101, an invention must have a specific, substantial, and credible utility, which is disclosed in the specification, or which is well established as considered by one of ordinary skill in the art. While MAFBX is described as being linked to muscle atrophy and other wasting diseases, no specific and/or substantial utility has been set forth in the specification (or the art) that constitutes a real-world use for the claimed nucleic acid molecules. Thus, the instant claims lack a patentable utility.

Claims 1-3, 5-8, and 33-40 are also rejected under 35 U.S.C. § 112, first paragraph, enablement. Specifically, since the claimed invention is not supported by either a specific and/or

substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claim Rejections - 35 U.S.C. § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. § 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

21. Claims 1-3, 5-8, and 33-40 are rejected under 35 U.S.C. § 102(a) as being anticipated by Yue *et al.* (WO 00/70047). The instant claims are drawn to polynucleotides encoding SEQ ID NO:35 and related products.

Yue *et al.* teach sequence 106 which exactly encodes SEQ ID NO:35 and a portion of which is identical to SEQ ID NO:34 (see attached alignments). Yue *et al.* also teach expression vectors and host cells (see Abstract).

22. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 102(e) as being anticipated by Goldberg *et al.* (USPAP 2003/0077288). The instant claims are drawn to polynucleotides similar to nucleic acid sequences encoding SEQ ID NO:35 and related products.

Goldberg *et al.* teach a nucleic acid molecule encoding mouse atrophin-1, an F-box protein related to muscle wasting (see Abstract and page 4). Said nucleic acid molecule encodes

a protein that is about 97% identical to SEQ ID NO:35 and is 90% identical to SEQ ID NO:34 (see attached alignment). Goldberg *et al.* teach expression systems in host cells (see page 2).

23. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 102(e) as being anticipated by Rosen *et al.* (USPAP 2002/0151681). The instant claims are drawn to polynucleotides similar to nucleic acid sequences encoding SEQ ID NO:35 and related products.

Rosen *et al.* teach SEQ ID NO:66, which is 82% identical to SEQ ID NO:34, and which encodes a protein that is 80% identical to SEQ ID NO:35. SEQ ID NO:66 almost exactly encodes residues 62-355 of SEQ ID NO:35 (missing the N-terminus) (see attached alignment). The Examiner notes that SEQ ID NO:66 has priority to at least March 8, 2000 by way of PCT/US00/05988 (WO 200055174). Rosen *et al.* also teach expression systems in host cells (see Abstract).

24. Claims 2, 3, 5-8, and 33-36 are rejected under 35 U.S.C. § 102(e) as being anticipated by Tang *et al.* (USPN 6,569,662). The instant claims are drawn to polynucleotides similar to nucleic acid sequences encoding SEQ ID NO:35 and related products.

Tang *et al.* teach SEQ ID NO:1011, which is 61% identical to SEQ ID NO:34, and which encodes a protein that is 60% identical to SEQ ID NO:35. SEQ ID NO:1011 almost exactly encodes residues 1-217 of SEQ ID NO:35 (missing the C-terminus) (see attached alignment). Tang *et al.* also teach expression systems in host cells (see column 3).

Conclusion

25. Claims 1-3, 5-8, and 33-40 are not allowed for the reasons identified in the numbered sections of this Office action. Applicants must respond to the objections/rejections in each of the numbered sections in this Office action to be fully responsive in prosecution.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Kathleen M Kerr whose telephone number is (571) 272-0931. The examiner can normally be reached on Monday through Friday, from 9:00am to 6pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathupura Achutamurthy can be reached on (571) 272-0928. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Kathleen M Kerr
Examiner
Art Unit 1652

April 14, 2004

ALIGNMENT

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LOCUS       AR339520                828 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1011 from patent US 6569662.
ACCESSION   AR339520
VERSION     AR339520.1  GI:33726377
REFERENCE   1  (bases 1 to 828)
  AUTHORS   Tang,Y.T., Zhou,P. and Drmanac,R.T.
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: US 6569662-A 1011 27-MAY-2003;

  Query Match             61.0%;  Score 649.4;  DB 6;  Length 828;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-152;
  Matches  650;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCCGGGCAGAACTGGGTGAAGACGGCCGAC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         45 ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCGGGGCAGAACTGGGTGAAGACGGCCGAC 104

Qy         61 GGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 GGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC 164

Qy        121 TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACTATGATGTTGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACTATGATGTTGCA 224

Qy        181 GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAAACTCAGTATTTCCACCAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAAACTCAGTATTTCCACCAA 284

Qy        241 GAAAAATGGATCTATGTTCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GAAAAATGGATCTATGTTCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG 344

Qy        301 GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC 404

Qy        361 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 464

Qy        421 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 524

Qy        481 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 584

Qy        541 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 644

Qy        601 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGG 651
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGG 695
```

; Sequence 1011, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and Polypeptides
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SEQ ID NO 1011
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(809)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(828)
; OTHER INFORMATION: n = a,t,c or g
US-09-620-312D-1011

Alignment Scores:

Pred. No.:	3.06e-130	Length:	828
Score:	1136.00	Matches:	217
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	60.07%	Indels:	0
DB:	4	Gaps:	0

US-10-061-043A-35 (1-355) x US-09-620-312D-1011 (1-828)

```
Qy          1 MetProPheLeuGlyGlnAspTrpArgSerProGlyGlnAsnTrpValLysThrAlaAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         45 ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCGGGGCAGAACTGGGTGAAGACGGCCGAC 104

Qy         21 GlyTrpLysArgPheLeuAspGluLysSerGlySerPheValSerAspLeuSerSerTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 GGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC 164

Qy         41 CysAsnLysGluValTyrAsnLysGluAsnLeuPheAsnSerLeuAsnTyrAspValAla 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACTATGATGTTGCA 224

Qy         61 AlaLysLysArgLysLysAspMetLeuAsnSerLysThrLysThrGlnTyrPheHisGln 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAAACTCAGTATTTCCACCAA 284

Qy         81 GluLysTrpIleTyrValHisLysGlySerThrLysGluArgHisGlyTyrCysThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GAAAAATGGATCTATGTTCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG 344

Qy        101 GlyGluAlaPheAsnArgLeuAspPheSerThrAlaIleLeuAspSerArgArgPheAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        345 GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC 404
```

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Qy        121 TyrValValArgLeuLeuGluLeuIleAlaLysSerGlnLeuThrSerLeuSerGlyIle 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 464

Qy        141 AlaGlnLysAsnPheMetAsnIleLeuGluLysValValLeuLysValLeuGluAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 524

Qy        161 GlnAsnIleArgLeuIleArgGluLeuLeuGlnThrLeuTyrThrSerLeuCysThrLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        525 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 584

Qy        181 ValGlnArgValGlyLysSerValLeuValGlyAsnIleAsnMetTrpValTyrArgMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 644

Qy        201 GluThrIleLeuHisTrpGlnGlnGlnLeuAsnAsnIleGlnIleThrArg 217
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGG 695
```

ALIGNMENT

ID AAF15631 standard; cDNA; 1302 BP.
XX
AC AAF15631;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:66.
XX
OS Homo sapiens.
XX
PN WO200055174-A1. = PCT/US00/05988
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
SQ Sequence 1302 BP; 400 A; 297 C; 295 G; 307 T; 0 U; 3 Other;

LATER filed USPAP 2002/0151681

Query Match 81.6%; Score 868.6; DB 3; Length 1302;
Best Local Similarity 99.3%; Pred. No. 1.9e-244;
Matches 879; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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Qy        181 GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAAACTCAGTATTTCCACCAA 240
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 GACAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAAACTCAGTATTTCCACCAG 64

Qy        241 GAAAAATGGATCTATGTTCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG 300
              ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db         65 GAAAAATGGATCTATGTTCACAAAGGAAGTACTAMAGAGCGCCATGGATATTGCACCCTG 124

Qy        301 GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC 360
              |||:||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db        125 GGGRAAGCTTTCAACAGACTGGACTTCTCAACTGCMATTCTGGATTCCAGAAGATTTAAC 184

Qy        361 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 244

Qy        421 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 304

Qy        481 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 364

Qy        541 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        365 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 424
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Qy        601 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTC 484

Qy        661 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTG 544

Qy        721 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCCGACCTGCACGTGCTCAGC 780
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        545 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCA-GCTGCCCCCGACCTGCACGTGCTCAGC 603

Qy        781 GAAGACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGAGCGGCAGATCCGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 GAAGACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGAGCGGCAGATCCGC 663

Qy        841 AAACGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AAACGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACTT 723

Qy        901 GTCCGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 GTCCGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGT 783

Qy        961 CACATCCTTTCCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 CACATCCTTTCCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGC 843

Qy       1021 TCCGTTTCACTTTCACCCCAGGACTTTATCAACTTGTTCAAGTTC 1065
              |||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCGTTTCACTTTCACCCCAGGACTTTATCAACTTGTTCAAGTTC 888
```

ID AAF15631 standard; cDNA; 1302 BP.
XX
AC AAF15631;
XX
DT 13-MAR-2001 (first entry)
XX
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:66.
XX
OS Homo sapiens.
XX
PN WO200055174-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005988.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX
PI Rosen CA, Ruben SM;
XX
SQ Sequence 1302 BP; 400 A; 297 C; 295 G; 307 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.:	1.31e-150	Length:	1302
Score:	1515.00	Matches:	291
Percent Similarity:	98.98%	Conservative:	0
Best Local Similarity:	98.98%	Mismatches:	3
Query Match:	80.12%	Indels:	1
DB:	3	Gaps:	0

US-10-061-043A-35 (1-355) x AAF15631 (1-1302)

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Qy          62 LysLysArgLysLysAspMetLeuAsnSerLysThrLysThrGlnTyrPheHisGlnGlu 81
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           8 AAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAAACTCAGTATTTCCACCAGGAA 67

Qy          82 LysTrpIleTyrValHisLysGlySerThrLysGluArgHisGlyTyrCysThrLeuGly 101
               |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db          68 AAATGGATCTATGTTCACAAAGGAAGTACTAMAGAGCGCCATGGATATTGCACCCTGGGG 127

Qy         102 GluAlaPheAsnArgLeuAspPheSerThrAlaIleLeuAspSerArgArgPheAsnTyr 121
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         128 RAAGCTTTCAACAGACTGGACTTCTCAACTGCMATTCTGGATTCCAGAAGATTTAACTAC 187

Qy         122 ValValArgLeuLeuGluLeuIleAlaLysSerGlnLeuThrSerLeuSerGlyIleAla 141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         188 GTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATCGCC 247

Qy         142 GlnLysAsnPheMetAsnIleLeuGluLysValValLeuLysValLeuGluAspGlnGln 161
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         248 CAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAGCAA 307
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Qy        162 AsnIleArgLeuIleArgGluLeuLeuGlnThrLeuTyrThrSerLeuCysThrLeuVal 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 AACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTGGTC 367

Qy        182 GlnArgValGlyLysSerValLeuValGlyAsnIleAsnMetTrpValTyrArgMetGlu 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 CAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATGGAG 427

Qy        202 ThrIleLeuHisTrpGlnGlnGlnLeuAsnAsnIleGlnIleThrArgProAlaPheLys 221
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 ACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTCAAA 487

Qy        222 GlyLeuThrPheThrAspLeuProLeuCysLeuGlnLeuAsnIleMetGlnArgLeuSer 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 GGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTGAGC 547

Qy        242 AspGlyArgAspLeuValSerLeuGlyGlnAlaAlaProAspLeuHisValLeuSerGlu 261
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        548 GACGGGCGGGACCTGGTCAGCCTGGGCCAGCT-GCCCCCGACCTGCACGTGCTCAGCGAA 606

Qy        262 AspArgLeuLeuTrpLysLysLeuCysGlnTyrHisPheSerGluArgGlnIleArgLys 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGAGCGGCAGATCCGCAAA 666

Qy        282 ArgLeuIleLeuSerAspLysGlyGlnLeuAspTrpLysLysMetTyrPheLysLeuVal 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACTTGTC 726

Qy        302 ArgCysTyrProArgLysGluGlnTyrGlyAspThrLeuGlnLeuCysLysHisCysHis 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 CGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGTCAC 786

Qy        322 IleLeuSerTrpLysGlyThrAspHisProCysThrAlaAsnAsnProGluSerCysSer 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 ATCCTTTCCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGCTCC 846

Qy        342 ValSerLeuSerProGlnAspPheIleAsnLeuPheLysPhe 355
              |||||||||||||||||||||||||||||||||||||||||||
Db        847 GTTTCACTTTCACCCCAGGACTTTATCAACTTGTTCAAGTTC 888
```

ALIGNMENT

ID ADE24728 standard; cDNA; 2067 BP.
XX
AC ADE24728;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse cDNA encoding F-box protein, Atrophin-1.
XX
OS Mus sp.
XX
PN US2003077288-A1.
XX
PD 24-APR-2003.
XX
PF 16-JAN-2002; 2002US-00050686.
XX
PR 16-JAN-2001; 2001US-0262090P.
XX
PI Goldberg AL, Gomes MD, Lecker SH, Jagoe RT;
XX
SQ Sequence 2067 BP; 572 A; 512 C; 527 G; 456 T; 0 U; 0 Other;

Query Match 90.2%; Score 961; DB 9; Length 2067;
Best Local Similarity 93.9%; Pred. No. 1.6e-271;
Matches 1000; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Qy          1 ATGCCATTCCTCGGGCAGGACTGGCGGTCCCCCGGGCAGAACTGGGTGAAGACGGCCGAC 60
              ||||| ||||| |||||||||||||||||||| || |||| |||||||||||||| |||
Db        328 ATGCCGTTCCTTGGGCAGGACTGGCGGTCCCCGGGCCAGAGCTGGGTGAAGACGGCGGAC 387

Qy         61 GGCTGGAAGCGCTTCCTGGATGAGAAGAGCGGCAGTTTCGTGAGCGACCTCAGCAGTTAC 120
              |||||||||||||||| |||||||||| |||||||| |||||||||||||||||||||||
Db        388 GGCTGGAAGCGCTTCTTGGATGAGAAAAGCGGCAGCTTCGTGAGCGACCTCAGCAGTTAC 447

Qy        121 TGCAACAAGGAGGTATACAATAAGGAGAATCTTTTCAACAGCCTGAACTATGATGTTGCA 180
              |||||||||||||||||||| |||||||||||| |||| ||||||| |||| || || |||
Db        448 TGCAACAAGGAGGTATACAGTAAGGAGAATCTGTTCAGCAGCCTGGACTACGACGTCGCA 507

Qy        181 GCCAAGAAGAGAAAGAAGGACATGCTGAATAGCAAAACCAAAACTCAGTATTTCCACCAA 240
              |||||||||||||||||| ||||| | ||| ||||||||||||||||||| ||||| |||
Db        508 GCCAAGAAGAGAAAGAAAGACATTCAGAACAGCAAAACCAAAACTCAGTACTTCCATCAA 567

Qy        241 GAAAAATGGATCTATGTTCACAAAGGAAGTACTAAAGAGCGCCATGGATATTGCACCCTG 300
              ||||| |||||||||||||||||||||||| || |||||||||||||| || ||  ||
Db        568 GAAAAGTGGATCTATGTTCACAAAGGAAGTACGAAGGAGCGCCATGGATACTGTACTTTG 627

Qy        301 GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC 687

Qy        361 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 747

Qy        421 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 807
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Qy        481 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 867

Qy        541 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 927

Qy        601 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTC 987

Qy        661 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTG 1047

Qy        721 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCTGCCCCCGACCTGCACGTGCTCAGC 780
              |||||||||||||||||||||||||||||||| ||||| |||||||| ||||||||
Db       1048 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCAGCCCCAGACCTGCATGTGCTCAGT 1107

Qy        781 GAAGACCGGCTGCTGTGGAAGAAACTCTGCCAGTACCACTTCTCCGAGCGGCAGATCCGC 840
              || |||||||| |||||||||| ||||||||||||||||||||| ||| ||||||| |||
Db       1108 GAGGACCGGCTACTGTGGAAGAGACTCTGCCAGTACCACTTCTCAGAGAGGCAGATTCGC 1167

Qy        841 AAACGATTAATTCTGTCAGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTCAAACTT 900
              || || || ||  |||| ||||||||||||||||||||||||||||||||| || |||
Db       1168 AAGCGTTTGATCTTGTCTGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTTAAGCTT 1227

Qy        901 GTCCGATGTTACCCAAGGAAAGAGCAGTATGGAGATACCCTTCAGCTCTGCAAACACTGT 960
              || |||||||||||||| | |||||||||||| |  ||||| ||||| ||||||||||
Db       1228 GTACGATGTTACCCAAGAAGAGAGCAGTATGGGGTCACCCTGCAGCTTTGCAAACACTGC 1287

Qy        961 CACATCCTTTCCTGGAAGGGCACTGACCATCCGTGCACTGCCAATAACCCAGAGAGCTGC 1020
              ||||| || |||||||||||||||||||||||||||| ||||| ||||||||||||||
Db       1288 CACATTCTCTCCTGGAAGGGCACTGACCATCCGTGCACGGCCAACAACCCAGAGAGCTGC 1347

Qy       1021 TCCGTTTCACTTTCACCCCAGGACTTTATCAACTTGTTCAAGTTC 1065
              ||||| |||||||| || || |||||||||| ||||||||||
Db       1348 TCCGTCTCACTTTCCCCTCAAGACTTTATCAATTTGTTCAAGTTC 1392
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ID ADE24728 standard; cDNA; 2067 BP.
XX
AC ADE24728;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse cDNA encoding F-box protein, Atrophin-1.
XX
OS Mus sp.
XX
PN US2003077288-A1.
XX
PD 24-APR-2003.
XX
PF 16-JAN-2002; 2002US-00050686.
XX
PR 16-JAN-2001; 2001US-0262090P.
XX
PI Goldberg AL, Gomes MD, Lecker SH, Jagoe RT;
XX
SQ Sequence 2067 BP; 572 A; 512 C; 527 G; 456 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.92e-185	Length:	2067
Score:	1846.00	Matches:	346
Percent Similarity:	99.44%	Conservative:	7
Best Local Similarity:	97.46%	Mismatches:	2
Query Match:	97.62%	Indels:	0
DB:	9	Gaps:	0

US-10-061-043A-35 (1-355) x ADE24728 (1-2067)

```
Qy          1 MetProPheLeuGlyGlnAspTrpArgSerProGlyGlnAsnTrpValLysThrAlaAsp 20
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        328 ATGCCGTTCCTTGGGCAGGACTGGCGGTCCCCGGGCCAGAGCTGGGTGAAGACGGCGGAC 387

Qy         21 GlyTrpLysArgPheLeuAspGluLysSerGlySerPheValSerAspLeuSerSerTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 GGCTGGAAGCGCTTCTTGGATGAGAAAAGCGGCAGCTTCGTGAGCGACCTCAGCAGTTAC 447

Qy         41 CysAsnLysGluValTyrAsnLysGluAsnLeuPheAsnSerLeuAsnTyrAspValAla 60
              ||||||||||||||||:::||||||||||||||:::|||||||:::||||||||||||
Db        448 TGCAACAAGGAGGTATACAGTAAGGAGAATCTGTTCAGCAGCCTGGACTACGACGTCGCA 507

Qy         61 AlaLysLysArgLysLysAspMetLeuAsnSerLysThrLysThrGlnTyrPheHisGln 80
              ||||||||||||||||||||||:::   ||||||||||||||||||||||||||||||||
Db        508 GCCAAGAAGAGAAAGAAAGACATTCAGAACAGCAAAACCAAAACTCAGTACTTCCATCAA 567

Qy         81 GluLysTrpIleTyrValHisLysGlySerThrLysGluArgHisGlyTyrCysThrLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        568 GAAAAGTGGATCTATGTTCACAAAGGAAGTACGAAGGAGCGCCATGGATACTGTACTTTG 627

Qy        101 GlyGluAlaPheAsnArgLeuAspPheSerThrAlaIleLeuAspSerArgArgPheAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        628 GGGGAAGCTTTCAACAGACTGGACTTCTCAACTGCCATTCTGGATTCCAGAAGATTTAAC 687
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Qy        121 TyrValValArgLeuLeuGluLeuIleAlaLysSerGlnLeuThrSerLeuSerGlyIle 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        688 TACGTGGTCCGGCTGTTGGAGCTGATAGCAAAGTCACAGCTCACATCCCTGAGTGGCATC 747

Qy        141 AlaGlnLysAsnPheMetAsnIleLeuGluLysValValLeuLysValLeuGluAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 GCCCAAAAGAACTTCATGAATATTTTGGAAAAAGTGGTACTGAAAGTCCTTGAAGACCAG 807

Qy        161 GlnAsnIleArgLeuIleArgGluLeuLeuGlnThrLeuTyrThrSerLeuCysThrLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 CAAAACATTAGACTAATAAGGGAACTACTCCAGACCCTCTACACATCCTTATGTACACTG 867

Qy        181 ValGlnArgValGlyLysSerValLeuValGlyAsnIleAsnMetTrpValTyrArgMet 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GTCCAAAGAGTCGGCAAGTCTGTGCTGGTCGGGAACATTAACATGTGGGTGTATCGGATG 927

Qy        201 GluThrIleLeuHisTrpGlnGlnGlnLeuAsnAsnIleGlnIleThrArgProAlaPhe 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 GAGACGATTCTCCACTGGCAGCAGCAGCTGAACAACATTCAGATCACCAGGCCTGCCTTC 987

Qy        221 LysGlyLeuThrPheThrAspLeuProLeuCysLeuGlnLeuAsnIleMetGlnArgLeu 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AAAGGCCTCACCTTCACTGACCTGCCTTTGTGCCTACAACTGAACATCATGCAGAGGCTG 1047

Qy        241 SerAspGlyArgAspLeuValSerLeuGlyGlnAlaAlaProAspLeuHisValLeuSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 AGCGACGGGCGGGACCTGGTCAGCCTGGGCCAGGCAGCCCCAGACCTGCATGTGCTCAGT 1107

Qy        261 GluAspArgLeuLeuTrpLysLysLeuCysGlnTyrHisPheSerGluArgGlnIleArg 280
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       1108 GAGGACCGGCTACTGTGGAAGAGACTCTGCCAGTACCACTTCTCAGAGAGGCAGATTCGC 1167

Qy        281 LysArgLeuIleLeuSerAspLysGlyGlnLeuAspTrpLysLysMetTyrPheLysLeu 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 AAGCGTTTGATCTTGTCTGACAAAGGGCAGCTGGATTGGAAGAAGATGTATTTTAAGCTT 1227

Qy        301 ValArgCysTyrProArgLysGluGlnTyrGlyAspThrLeuGlnLeuCysLysHisCys 320
              ||||||||||||||||||:::|||||||||||   ||||||||||||||||||||||||
Db       1228 GTACGATGTTACCCAAGAAGAGAGCAGTATGGGGTCACCCTGCAGCTTTGCAAACACTGC 1287

Qy        321 HisIleLeuSerTrpLysGlyThrAspHisProCysThrAlaAsnAsnProGluSerCys 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 CACATTCTCTCCTGGAAGGGCACTGACCATCCGTGCACGGCCAACAACCCAGAGAGCTGC 1347

Qy        341 SerValSerLeuSerProGlnAspPheIleAsnLeuPheLysPhe 355
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1348 TCCGTCTCACTTTCCCCTCAAGACTTTATCAATTTGTTCAAGTTC 1392
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